Table V1: Summary of the ability of the candidate genes in classifying the validating strains into the Liti's cluster. Genes able to classify all but one strains were considered as validated.
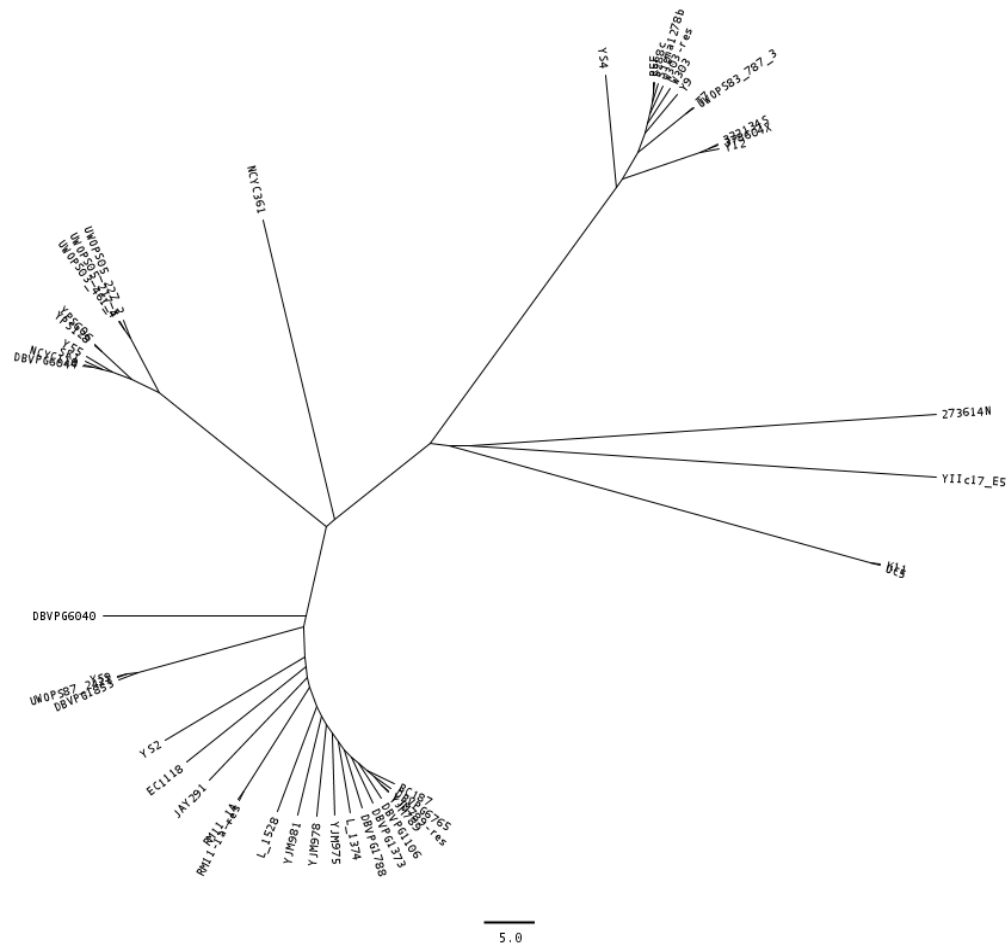
Cluster	W303	RM11-1a	JML-789	EC1118	Score
	Lab	WE	none	WE	
YBL052C	X	X	X	X	4
YBR163W		X	X	X	3
YJL051W	X	X	X	X	4
YKL068W	X	X	X	X	4
YML080W	X	X	X	X	4
YNL125C	X	X		X	3
YNL161W	X	X		X	3
YPR152C	X		X		2

X: validated; WE: Wine/European; Lab: laboratory strains

Figure V1: trees of the 47 S. cerevisiae strains (39 from the learning set plus 8 from the validation set) obtained with the YBL052C gene.

Figure V2: trees of the 47 *S. cerevisiae* strains (39 from the learning set plus 8 from the validation set) obtained with the YBR163W gene.
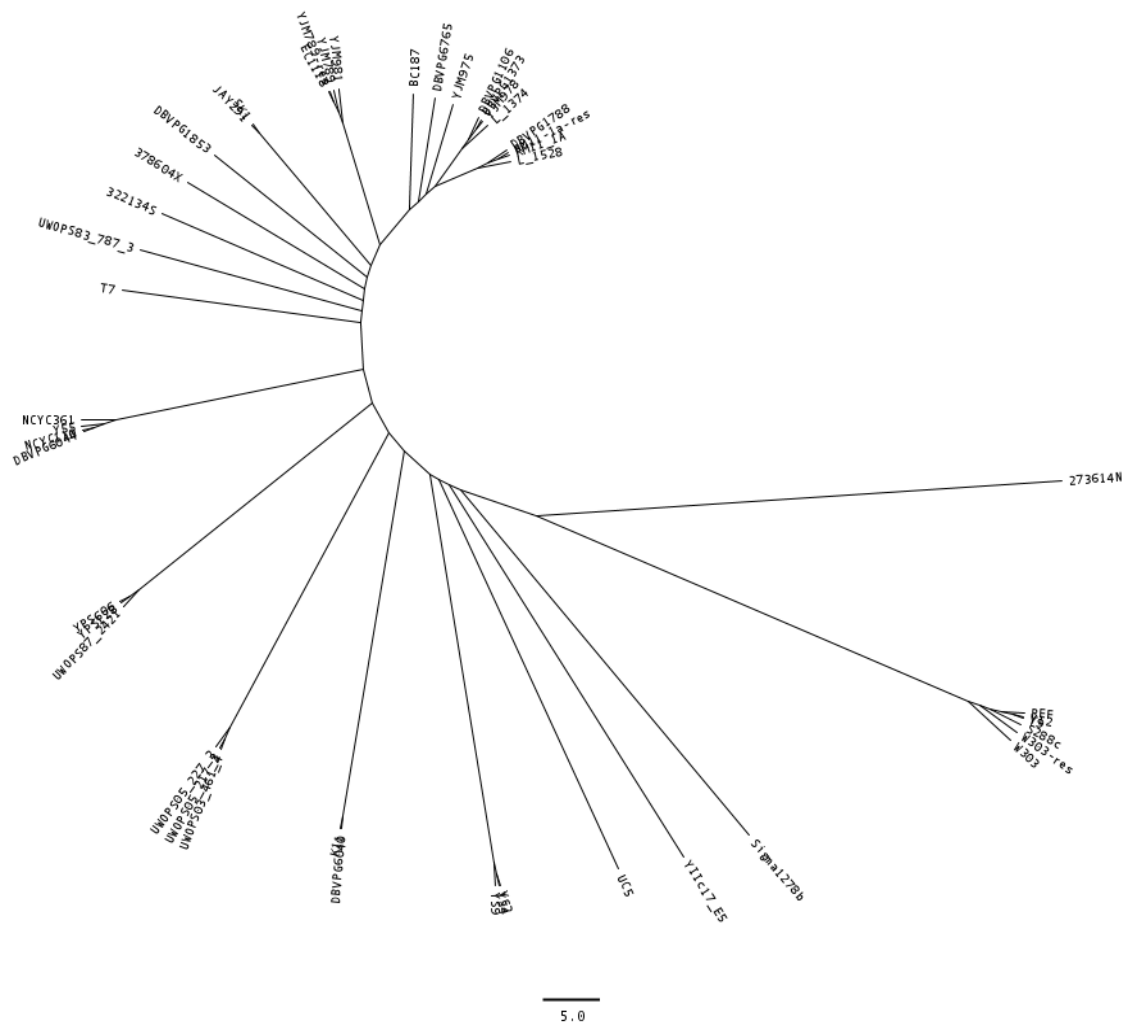
Figure V3: trees of the 47 S. cerevisiae strains (39 from the learning set plus 8 from the validation set) obtained with the YJL051W gene.

Figure V4: trees of the 47 S. cerevisiae strains (39 from the learning set plus 8 from the validation set) obtained with the YKL068W gene.
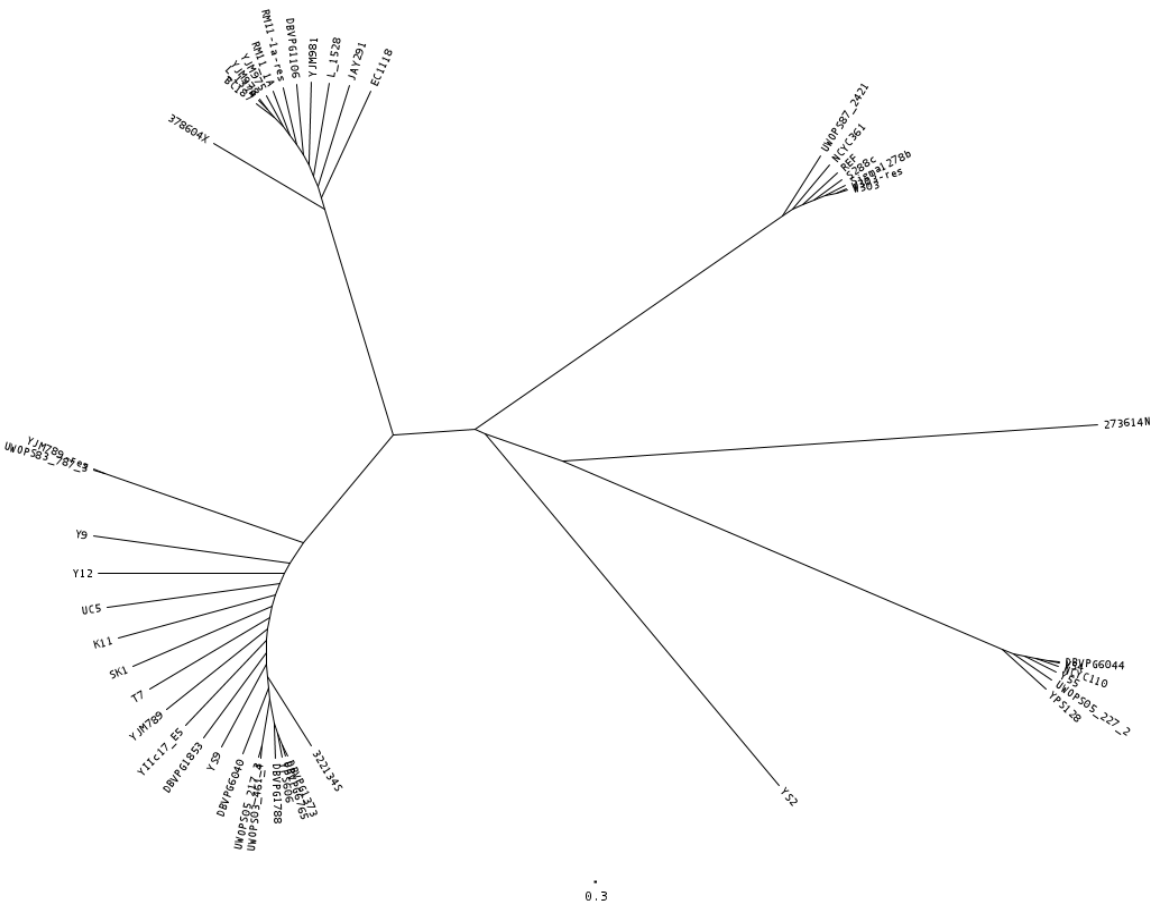
Figure V5: trees of the 47 S. cerevisiae strains (39 from the learning set plus 8 from the validation set) obtained with the YML080W gene.

Figure V6: trees of the 47 S. cerevisiae strains (39 from the learning set plus 8 from the validation set) obtained with the YNL125C gene.

Figure V7: trees of the 47 S. cerevisiae strains (39 from the learning set plus 8 from the validation set) obtained with the YNL161W gene.

Figure V8: trees of the 47 S. cerevisiae strains (39 from the learning set plus 8 from the validation set) obtained with the YPR152C gene.

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